CLAIM AMENDMENTS

1. (currently amended): A method to identify a desired region of a target nucleic acid to be targeted for observation, which method comprises

~~contacting~~ preparing a reaction mixture containing a sample containing said target nucleic acid and non-target nucleic acid with first and second probes that bracket said region, which first probe comprises a first oligomer specific for a sequence upstream of said region coupled to a first particulate label, and

said second probe comprises a second oligomer specific for a proximal sequence downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are observable by microscopy, **[[**~~and~~**]]**

displaying the reaction mixture on a surface under a microscope, and

observing ~~by microscopy~~ the presence or absence of ~~proximity~~ any pairs of the first and second particulate labels ~~to each other~~ as separate points in space, whereby the presence of said ~~proximity~~ pairs identifies said desired region**[[**,**]]**

~~wherein said method does not include a step of separating the target nucleic acid from non-target nucleic acid~~.

2. (previously presented): The method of claim 1, wherein said first and second particulate labels comprise first and second fluorophores.

3. (previously presented): The method of claim 2, wherein said first and second fluorophores are distinguishable from each other.

4. (original): The method of claim 1, wherein said first and second oligomers are peptide nucleic acids.

5. (original): The method of claim 1, wherein said target nucleic acid is single-stranded and said first and second oligomers are complementary to the upstream and downstream sequences bracketing said region.

6. (original): The method of claim 1, wherein said target nucleic acid is double-stranded and said first and second oligomers form triplexes with said upstream and downstream sequences bracketing said region.

7. (original): The method of claim 1, which is performed simultaneously on a multiplicity of target nucleic acids using a multiplicity of identification probes having particulate labels of differing hues coupled to oligomers comprising sequences complementary to a multiplicity of said upstream and downstream sequences bracketing a multiplicity of such regions.

8. (currently amended): A method to detect the presence of a target nucleic acid of known sequence, which method comprises

~~contacting~~ preparing a reaction mixture containing a sample to be tested for containing said target nucleic acid and further containing non-target nucleic acid with at least first and second probes that bracket a region of said target nucleic acid, which first probe comprises a first oligomer specific for a sequence upstream of said region coupled to a first particulate label and said second probe comprises a second oligomer specific for a proximal sequence downstream of said region coupled to a second particulate label;

wherein said first and second particulate labels are observable by microscopy, **[[**~~and~~**]]**

displaying the reaction mixture on a surface for microscope observation, and

observing ~~by microscopy~~ the presence or absence of ~~proximity~~ any pairs of the first and second particulate labels ~~to each other~~ as separate points in space, whereby the presence of said ~~proximity~~ pairs indicates the presence of said target nucleic acid**[[**,**]]**

~~wherein said method does not include a step of separating the target nucleic acid from non-target nucleic acid~~.

9. (previously presented): The method of claim 8, wherein said first and second particulate labels comprise first and second fluorophores.

10. (previously presented): The method of claim 9, wherein said first and second fluorophores are the same as each other.

11. (original): The method of claim 8, wherein said first and second oligomers are peptide nucleic acids.

12. (original): The method of claim 8, wherein said target nucleic acid is single-stranded and said first and second oligomers are complementary to the upstream and downstream sequences bracketing said region.

13. (original): The method of claim 8, wherein said target nucleic acid is double-stranded and said first and second oligomers form triplexes with said upstream and downstream sequences bracketing said region.

14. (original): The method of claim 8, which is performed simultaneously on a multiplicity of target nucleic acids, using a multiplicity of identification probes having particulate labels of differing hues for each known sequence targeted coupled to oligomers with different specificities according to the sequences targeted.

15. (original): The method of claim 8, wherein said target nucleic acid of known sequence is derived from an organism.

16. (original): The method of claim 15, wherein the organism is an infectious agent.

17. (original): The method of claim 15, wherein the organism is a human subject.

18-47. (canceled)